Notice of Allowability	Application No.	Applicant(s)	
	09/900,237	ALLEN, STEPHEN M.	
	Examiner	Art Unit	
	Phuong T. Bui	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address--

All claims being allowable, PROSECUTION ON THE MERITS IS (OR REMAINS) CLOSED in this application. If not included herewith (or previously mailed), a Notice of Allowance (PTOL-85) or other appropriate communication will be mailed in due course. **THIS NOTICE OF ALLOWABILITY IS NOT A GRANT OF PATENT RIGHTS.** This application is subject to withdrawal from issue at the initiative of the Office or upon petition by the applicant. See 37 CFR 1.313 and MPEP 1308.

1. ☒ This communication is responsive to *RCE filed 4/15/04*.

2. ☒ The allowed claim(s) is/are *23 and 27-35*.

3. ☒ The drawings filed on 10/27/03 are accepted by the Examiner.

4. ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
   a) ☐ All b) ☐ Some* c) ☐ None of the:
      1. ☐ Certified copies of the priority documents have been received.
      2. ☐ Certified copies of the priority documents have been received in Application No. _____ .
      3. ☐ Copies of the certified copies of the priority documents have been received in this national stage application from the International Bureau (PCT Rule 17.2(a)).

   * Certified copies not received: _____.

Applicant has THREE MONTHS FROM THE "MAILING DATE" of this communication to file a reply complying with the requirements noted below. Failure to timely comply will result in ABANDONMENT of this application.
THIS THREE-MONTH PERIOD IS NOT EXTENDABLE.

5. ☐ A SUBSTITUTE OATH OR DECLARATION must be submitted. Note the attached EXAMINER'S AMENDMENT or NOTICE OF INFORMAL PATENT APPLICATION (PTO-152) which gives reason(s) why the oath or declaration is deficient.

6. ☐ CORRECTED DRAWINGS (as "replacement sheets") must be submitted.
   (a) ☐ including changes required by the Notice of Draftsperson's Patent Drawing Review (PTO-948) attached
      1) ☐ hereto or 2) ☐ to Paper No./Mail Date _____.
   (b) ☐ including changes required by the attached Examiner's Amendment / Comment or in the Office action of Paper No./Mail Date _____.

   Identifying indicia such as the application number (see 37 CFR 1.84(c)) should be written on the drawings in the front (not the back) of each sheet. Replacement sheet(s) should be labeled as such in the header according to 37 CFR 1.121(d).

7. ☐ DEPOSIT OF and/or INFORMATION about the deposit of BIOLOGICAL MATERIAL must be submitted. Note the attached Examiner's comment regarding REQUIREMENT FOR THE DEPOSIT OF BIOLOGICAL MATERIAL.

Attachment(s)

1. ☒ Notice of References Cited (PTO-892)
2. ☐ Notice of Draftperson's Patent Drawing Review (PTO-948)
3. ☒ Information Disclosure Statements (PTO-1449 or PTO/SB/08), Paper No./Mail Date 4/15/04
4. ☐ Examiner's Comment Regarding Requirement for Deposit of Biological Material
5. ☐ Notice of Informal Patent Application (PTO-152)
6. ☒ Interview Summary (PTO-413), Paper No./Mail Date *9/3//04* .
7. ☒ Examiner's Amendment/Comment
8. ☒ Examiner's Statement of Reasons for Allowance
9. ☐ Other _____.

EXAMINER'S AMENDMENT

1. An examiner's amendment to the record appears below. Should the changes and/or additions be unacceptable to applicant, an amendment may be filed as provided by 37 CFR 1.312. To ensure consideration of such an amendment, it MUST be submitted no later than the payment of the issue fee.

Authorization for this examiner's amendment was given in a telephone interview with Kenneth Joung on September 3, 2004.

The application has been amended as follows:

In claim 23, line 4, "90%" was amended to –95%--.

Claim 26 has been canceled.

REASONS FOR ALLOWANCE

2. The following is an examiner's statement of reasons for allowance: Applicant's earliest filing date for SEQ ID NO:29 encoding SEQ ID NO:30 is July 6, 2001. The prior art teaches a sequence having 94.1% (WO2003000898 (N)), 93.9% (WO200179516 (O)), and 93.8% (WO200009706 (P)) sequence identity with Applicant's SEQ ID NO:30. A copy of the PCT documents will not be sent to Applicant, as the Office believes the attached sequence search results from database N_Geneseq will provide Applicant more useful percent sequence identity information. Because the prior art does not teach or fairly suggest a sequence having 95% sequence identity with Applicant's claimed sequence at the amino acid level, the claimed invention is free of the prior art.

3. Any comments considered necessary by applicant must be submitted no later than the payment of the issue fee and, to avoid processing delays, should preferably

accompany the issue fee. Such submissions should be clearly labeled "Comments on Statement of Reasons for Allowance."

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Phuong T. Bui whose telephone number is 571-272-0793. The examiner can normally be reached on Monday-Friday.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Amy Nelson can be reached on 571-272-0804. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Phuong T. Bui
Primary Examiner
Art Unit 1638

9/4/04

9/4/04

Please attach to Examiner's Amdt

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 22, 2004, 13:37:22 ; Search time 935 Seconds
(without alignments)
4907.010 Million cell updates/sec

Title: US-09-900-237A-30
Perfect score: 5778
Sequence: 1 MDGDADALKSGRHGAGDVCQ.....VDPFTTRLAGPNIQTCGINC 1080

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09900237/runat_18082004_081513_14627/app_query.fasta_1.1223
-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09900237_@CGN_1_1_649_@runat_18082004_081513_14627 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5434.5	94.1	3264	7	ADA69779	Ada69779 Rice gene
2	5423.5	93.9	3799	6	AAS16458	Aas16458 Corn cDNA
3	5421.5	93.8	3746	3	AAZ99512	Aaz99512 DNA encod
4	5421.5	93.8	3746	3	AAZ99527	Aaz99527 DNA encod
5	5421.5	93.8	3773	3	AAZ99494	Aaz99494 DNA encod
6	5169.5	89.5	3222	7	ADA69499	Ada69499 Rice gene
7	5143	89.0	3704	3	AAZ99533	Aaz99533 DNA encod
8	4530	78.4	3198	3	AAC49550	Aac49550 Arabidops
9	4499	77.9	3614	2	AAV06567	Aav06567 Arabidops
10	3993.5	69.1	3725	3	AAZ99500	Aaz99500 DNA encod
11	3993.5	69.1	3725	3	AAZ99521	Aaz99521 DNA encod
12	3993.5	69.1	3725	3	AAZ99506	Aaz99506 DNA encod
13	3981	68.9	3753	3	AAZ99530	Aaz99530 DNA encod
14	3981	68.9	3753	3	AAZ99515	Aaz99515 DNA encod
15	3981	68.9	3780	3	AAZ99497	Aaz99497 DNA encod
16	3963.5	68.6	3603	2	AAV06565	Aav06565 Arabidops
17	3953.5	68.4	3673	2	AAV06568	Aav06568 Arabidops
18	3939	68.2	3851	3	AAA67114	Aaa67114 Pinus rad
19	3844.5	66.5	3786	3	AAZ58265	Aaz58265 Corn cell
20	3844.5	66.5	3813	3	AAZ99509	Aaz99509 DNA encod
21	3844.5	66.5	3813	3	AAZ99524	Aaz99524 DNA encod
22	3820	66.1	3568	3	AAZ99491	Aaz99491 DNA encod
23	3818	66.1	3776	3	AAZ58263	Aaz58263 Corn cell
24	3818	66.1	3936	3	AAZ58266	Aaz58266 Corn cell
25	3818	66.1	3969	3	AAZ99518	Aaz99518 DNA encod
26	3818	66.1	3969	3	AAZ99503	Aaz99503 DNA encod
27	3807.5	65.9	3517	3	AAZ58268	Aaz58268 Soybean c
28	3777.5	65.4	3311	2	AAV08373	Aav08373 Cellulose
29	3666.5	63.5	3255	6	ABZ12754	Abz12754 Arabidops
30	3636	62.9	3255	6	ABZ14725	Abz14725 Arabidops
31	3633.5	62.9	3828	2	AAV06566	Aav06566 Arabidops
32	3583	62.0	3444	4	AAC83798	Aac83798 Arabidops
33	3535	61.2	2830	6	AAS16455	Aas16455 Corn cDNA
34	3518.5	60.9	8411	2	AAV06563	Aav06563 Arabidops
35	3514.5	60.8	7234	4	AAC83247	Aac83247 Cellulose
36	3482	60.3	3207	2	AAV08372	Aav08372 Cellulose
37	3477	60.2	3328	2	AAV34432	Aav34432 Cotton ce
38	3461.5	59.9	3747	3	AAA67145	Aaa67145 Eucalyptu
39	3337.5	57.8	3232	4	AAC65448	Aac65448 Populus t
40	3234	56.0	2890	3	AAZ58270	Aaz58270 Soybean c
41	2820	48.8	2306	2	AAV34433	Aav34433 Cotton ce
42	2689	46.5	1734	3	AAZ58271	Aaz58271 Wheat cel
43	2674	46.3	2033	2	AAV08381	Aav08381 Cellulose
44	2629.5	45.5	2248	2	AAV06562	Aav06562 Arabidops
45	2627.5	45.5	2125	3	AAZ58269	Aaz58269 Soybean c

ALIGNMENTS

RESULT 1
ADA69779
ID ADA69779 standard; DNA; 3264 BP.
XX
AC ADA69779;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 3102.
XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
XX
OS Oryza sativa.
XX
PN WO2003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
DR WPI; 2003-175290/17.
XX
PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to

PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
PS Claim 6; SEQ ID NO 3102; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 3264 BP; 784 A; 751 C; 852 G; 877 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	3264
Score:	5434.50	Matches:	998
Percent Similarity:	96.60%	Conservative:	52
Best Local Similarity:	91.81%	Mismatches:	30
Query Match:	94.06%	Indels:	7
DB:	7	Gaps:	2

US-09-900-237A-30 (1-1080) x ADA69779 (1-3264)

```
Qy          1 MetAspGlyAspAlaAspAlaLeuLysSerGlyArgHisGlyAlaGlyAspValCysGln 20
              ||||||||||||||||||||:::||||||||||||||||||:::|||     ||||||
Db          1 ATGGACGGCGACGCGGATGCCGTGAAGTCGGGGAGGCACGGGAGCGGGCAGGCGTGCCAG 60

Qy         21 IleCysAlaAspGlyLeuGlyThrThrLeuAspGlyAspValPheThrAlaCysAspVal 40
              ||||||   ||||||:::||||||||||   :::||||||||||||   ||||||||||||
Db         61 ATCTGCGGCGACGGCGTGGGCACGACGGCGGAGGGCGACGTGTTCGCCGCCTGCGACGTC 120

Qy         41 CysArgPheProValCysArgProCysTyrGluHisGluArgLysGluGlyThrGlnAla 60
              |||   ||||||||||||||||||||||||||:::||||||||:::||||||||||||||
Db        121 TGCGGCTTCCCGGTGTGCCGCCCCTGCTACGAGTACGAGCGCAAGGATGGCACCCAGGCT 180

Qy         61 CysLeuGlnCysLysThrLysTyrLysArgHisArgGlySerProAlaIleArgGlyGlu 80
              |||   ||||||||||||||||||||||||||:::||||||||:::||||||||||||||
Db        181 TGCCCCCAGTGCAAGACCAAGTACAAGCGCCACAAGGGGAGCCCGGCGATCCGTGGGGAG 240

Qy         81 GluGlyAspAspThrAspAlaAspAspGlySerAspPheAsnTyrProAlaSerGlyThr 100
              ||||||:::||||||||||||||||||   ||||||:::||||||||||||||||||:::
Db        241 GAAGGCGAGGATACTGATGCTGATGATGTCAGTGACTACAACTACCCTGCATCTGGCAGT 300

Qy        101 GluAspGlnLysGlnLysIleAlaAspArgMetArgSerTrpArgMetAsnThrGlyGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        301 GCCGACCAGAAGCAGAAGATTGCTGATAGGATGCGCAGTTGGCGCATGAATGCTGGGGGT 360

Qy        121 SerGlyAsnValGlyHisProLysTyrAspSerGlyGluIleGlyLeuSerLysTyrAsp 140
              |||:::||||||   ||||||||||||||||||||||||||||:::|||||||||||||
Db        361 GGTGGAGACGTCGGCCGTCCCAAGTATGACAGTGGCGAGATCGGGCTCACCAAGTATGAC 420

Qy        141 SerGlyGluIleProArgGlyTyrValProSerValThrAsnSerGlnMetSerGlyGlu 160
              ||||||||||||||||||||||:::||||||||||||||||||||:::|||||||||||
Db        421 AGTGGCGAGATCCCTCGGGGATACATCCCTTCAGTCACTAATAGCCAGATCTCGGGAGAA 480

Qy        161 IleProGlyAlaSerProAspHisHisMetMetSerProThrGlyAsnIleSerArgArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||   :::|||
Db        481 ATCCCTGGAGCTTCCCCTGATCATCATATGATGTCTCCTACCGGAAACATTGGCAAGCGT 540

Qy        181 AlaProPheProTyrValAsnHisSerProAsnProSerArgGluPheSerGlySerIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCTCCATTCCCCTATGTGAACCATTCACCAAATCCATCAAGGGAGTTCTCTGGCAGCATT 600

Qy        201 GlyAsnValAlaTrpLysGluArgValAspGlyTrpLysMetLysGlnAspLysGlyAla 220
              ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db        601 GGAAATGTTGCCTGGAAAGAAAGAGTTGATGGCTGGAAACTGAAGCAGGACAAGGGAGCA 660

Qy        221 IleProMetThrAsnGlyThrSerIleAlaProSerGluGlyArgAlaAlaThrAspIle 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTCCCATGACCAACGGGACAAGCATTGCCCCTTCTGAAGGTCGGGGAGTTGGTGATATC 720

Qy        241 AspAlaSerThrGluTyrAsnMetGluAspAlaLeuLeuAsnAspGluThrArgGlnPro 260
              ||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GATGCATCCACTGATTACAATATGGAAGATGCCTTACTGAATGATGAAACTCGCCAGCCT 780

Qy        261 LeuSerArgLysValProIleAlaSerSerLysIleAsnProTyrArgMetValIleVal 280
              ||||||||||||||||||:::   ||||||:::||||||||||||||||||||||||||
Db        781 CTCTCTAGAAAAGTTCCCCTTCCTTCATCCAGAATAAATCCCTACAGAATGGTCATTGTT 840

Qy        281 LeuArgLeuValValLeuSerIlePheLeuHisTyrArgLeuThrAsnProValArgAsn 300
              ||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||
Db        841 CTGCGTTTGGTTGTTCTAAGCATTTTCCTTCACTACCGTATTACGAATCCTGTGCGCAAT 900

Qy        301 AlaTyrProLeuTrpLeuLeuSerValIleCysGluIleTrpPheAlaLeuSerTrpIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCGTATCCGCTCTGGCTTTTATCTGTTATATGTGAGATTTGGTTTGCTTTGTCCTGGATA 960

Qy        321 LeuAspGlnPheProLysTrpPheProIleAsnArgGluThrTyrLeuAspArgLeuAla 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGGATCAGTTCCCGAAGTGGTTTCCAATCAACCGTGAAACCTACCTTGATAGGCTGGCA 1020

Qy        341 LeuArgTyrAspArgGluGlyGluProSerGlnLeuAlaAlaValAspIlePheValSer 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTGAGGTATGACAGAGAAGGTGAGCCATCTCAGTTGGCTGCTGTTGACATTTTTGTCAGT 1080

Qy        361 ThrValAspProLeuLysGluProProIleValThrAlaAsnThrValLeuSerIleLeu 380
              ||||||||||||:::||||||||||||:::||||||||||||||||||||||||||||||
Db       1081 ACAGTCGACCCCATGAAGGAACCTCCTCTTGTTACTGCCAATACCGTGCTGTCCATTCTT 1140

Qy        381 AlaValAspTyrProValAspLysValSerCysTyrValSerAspAspGlyAlaSerMet 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db       1141 GCTGTTGATTACCCAGTGGACAAGGTCTCTTGCTATGTATCTGACGATGGTGCTGCAATG 1200

Qy        401 LeuThrPheAspAlaLeuAlaGluThrSerGluPheAlaArgLysTrpValProPheVal 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CTGACTTTTGATGCATTGGCTGAGACTTCAGAGTTTGCTAGAAAGTGGGTTCCATTCGTT 1260

Qy        421 LysLysTyrAspIleGluProArgAlaProGluPheTyrPheCysGlnLysIleAspTyr 440
              |||||||||:::||||||||||||||||||||||||:::||||||    ||||||||||||
Db       1261 AAGAAGTATAACATTGAGCCAAGAGCTCCTGAGTGGTACTTCTCCCAGAAAATCGATTAC 1320

Qy        441 LeuLysAspLysValGlnProSerPheValLysAspArgArgAlaMetLysArgGluTyr 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTGAAAGACAAAGTCCACCCTTCATTTGTTAAAGACCGTCGTGCCATGAAGAGAGAATAT 1380

Qy        461 GluGluPheLysIleArgIleAsnAlaLeuValSerLysAlaLeuLysValProGluGlu 480
              ||||||||||||:::||||||||||   ||||||:::||||||   ||||||||||||||
Db       1381 GAAGAATTCAAAGTTAGGATAAATGGCCTTGTTGCTAAGGCACAGAAAGTCCCGGAGGAG 1440

Qy        481 GlyTrpIleMetGlnAspGlyThrProTrpProGlyAsnAsnThrArgAspHisProGly 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GGATGGATCATGCAAGATGGCACACCATGGCCAGGAAACAATACTAGGGACCATCCTGGA 1500

Qy        501 MetIleGlnValPheLeuGlyHisSerGlyGlyLeuAspThrGluGlyAsnGluLeuPro 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 ATGATTCAGGTTTTCCTTGGTCACAGTGGTGGCCTTGATACCGAGGGTAATGAGCTTCCC 1560

Qy        521 ArgLeuValTyrValSerArgGluLysArgProGlyPheGlnHisHisLysLysAlaGly 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CGCCTGGTCTACGTATCTCGTGAGAAGCGTCCTGGGTTTCAGCACCACAAGAAGGCTGGT 1620

Qy        541 AlaMetAsnAlaLeuValArgValSerAlaValLeuThrAsnGlyGlnTyrMetLeuAsn 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GCCATGAATGCTCTTGTTCGTGTCTCAGCTGTGCTTACCAATGGACAGTACATGTTGAAT 1680

Qy        561 LeuAspCysAspHisTyrIleAsnAsnSerLysAlaValArgGluAlaMetCysPheLeu 580
              ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db       1681 CTTGATTGTGATCACTACATCAACAACAGCAAGGCTCTGCGGGAAGCTATGTGCTTCCTT 1740

Qy        581 MetAspProAsnLeuGlyProGlnValCysTyrValGlnPheProGlnArgPheAspGly 600
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
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Db       1741 ATGGATCCAAACCTAGGAAGGAGTGTCTGTTATGTTCAGTTCCCACAAAGGTTCGATGGT 1800
Qy        601 IleAspArgAsnAspArgTyrAlaAsnArgAsnThrValPhePheAspIleAsnLeuArg 620
Db       1801 ATTGATAGGAATGATCGATATGCGAACAGGAACACTGTGTTTTTCGATATTAACTTGAGG 1860
Qy        621 GlyLeuAspGlyIleGlnGlyProValTyrValGlyThrGlyCysValPheAsnArgThr 640
Db       1861 GGTCTTGATGGCATCCAAGGACCAGTTTATGTGGGAACTGGTTGTGTATTCAACAGAACT 1920
Qy        641 AlaIleTyrGlyTyrGluProProIleLysAlaLysLysProGly---PheLeuAlaSer 659
Db       1921 GCTCTATATGGTTATGAACCCCCAATTAAGCAGAAGAAGAAGGGAAGTTTCTTGTCATCA 1980
Qy        660 LeuCysGlyGlyLysLysLysAlaSerLysSerLysLysArgSerSerAspLysLysLys 679
Db       1981 CTATGTGGGGGCAGGAAGAAGGCAAGCAAGTCAAAGAAGAAGAGTTCGGACAAGAAGAAG 2040
Qy        680 SerAsnLysHisValAspSerSerValProValPheAsnLeuGluAspIleGluGluGly 699
Db       2041 TCAAACAAGCACGTGGACAGTGCTGTGCCAGTTTTCAATCTTGAAGATATAGAGGAGGGT 2100
Qy        700 ValGluGlyAlaGlyPheAspAspGluLysSerValLeuMetSerGlnMetSerLeuGlu 719
Db       2101 GTTGAAGGTGCTGGATTCGATGATGAGAAATCACTTCTTATGTCTCAAATGAGCTTGGAG 2160
Qy        720 LysArgPheGlyGlnSerAlaAlaPheValAlaSerThrLeuMetGluTyrGlyGlyVal 739
Db       2161 AAGAGATTTGGCCAGTCTGCAGCGTTTGTTGCCTCCACTCTCATGGAATATGGTGGTGTT 2220
Qy        740 ProGlnSerSerThrProGluSerLeuLeuLysGluAlaIleHisValIleSerCysGly 759
Db       2221 CCTCAATCTGCAACCCCAGAATCTCTTTTGAAAGAAGCTATCCATGTGATAAGTTGTGGC 2280
Qy        760 TyrGluAspLysSerGluTrpGlyThrGlu----------IleGlyTrpIle 773
Db       2281 TATGAGGACAAGACCGAATGGGGAACTGAGGCTATGCAACTTGCAATGATTGGGTGGATC 2340
Qy        774 TyrGlySerValThrGluAspIleLeuThrGlyPheLysMetHisAlaArgGlyTrpArg 793
Db       2341 TACGGTTCCGTGACAGAAGATATTCTCACTGGATTCAAGATGCATGCGCGAGGCTGGAGA 2400
Qy        794 SerValTyrCysMetProLysArgProAlaPheLysGlySerAlaProIleAsnLeuSer 813
Db       2401 TCAATCTACTGCATGCCCAAGCGCCCAGCTTTCAAGGGGTCTGCTCCTATCAATCTTTCA 2460
Qy        814 AspArgLeuAsnGlnValLeuArgTrpAlaLeuGlySerValGluIleLeuPheSerArg 833
Db       2461 GATCGTCTTAACCAAGTGCTTCGGTGGGCACTTGGTTCTGTTGAAATTCTTTTCAGTCGC 2520
Qy        834 HisCysProLeuTrpTyrGlyTyrGlyGlyArgLeuLysPheLeuGluArgPheAlaTyr 853
Db       2521 CATTGTCCCATATGGTACGGCTATGGAGGACGCCTTAAGTTCTTGGAGAGATTTGCCTAC 2580
Qy        854 IleAsnThrThrIleTyrProLeuThrSerLeuProLeuLeuValTyrCysIleLeuPro 873
Db       2581 ATCAACACCACTATTTATCCATTGACATCGATCCCGCTTCTCATATACTGTGTTTTGCCT 2640
Qy        874 AlaIleCysLeuLeuThrGlyLysPheIleMetProGluIleSerAsnLeuAlaSerIle 893
Db       2641 GCTATCTGTTTGCTCACTGGGAAGTTCATCATCCCAGAGATTAGCAACTTTGCTAGTATT 2700
Qy        894 TrpPheIleAlaLeuPheLeuSerIlePheAlaThrGlyIleLeuGluMetArgTrpSer 913
Db       2701 TGGTTCATCTCTCTCTTCATTTCAATTTTTGCCACTGGTATCCTTGAGATGAGGTGGAGT 2760
Qy        914 GlyValGlyIleAspGluTrpTrpArgAsnGluGlnPheTrpValIleGlyGlyIleSer 933
Db       2761 GGTGTTGGCATCGATGAGTGGTGGAGGAATGAACAGTTCTGGGTTATTGGAGGTATATCT 2820
Qy        934 AlaHisLeuPheAlaValPheGlnGlyLeuLeuLysValLeuAlaGlyIleAspThrAsn 953
Db       2821 GCGCATCTTTTTGCCGTCTTCCAGGGTCTCCTCAAGGTGCTTGCTGGTATCGACACCAAT 2880

Qy        954 PheThrValThrSerLysAlaAsnAspGluGluGlyAspPheAlaGluLeuTyrMetPhe 973
Db       2881 TTCACTGTCACCTCAAAGGCTTCTGATGAAGATGGCGACTTTGCTGAGCTCTACATGTTC 2940
Qy        974 LysTrpThrThrLeuLeuIleProProThrThrIleLeuIleIleAsnMetValGlyVal 993
Db       2941 AAGTGGACAACGCTTCTCATCCCACCGACGACCATCTTGATCATTAACCTGGTCGGTGTT 3000
Qy        994 ValAlaGlyThrSerTyrAlaIleAsnSerGlyTyrGlnSerTrpGlyProLeuPheGly 1013
Db       3001 GTTGCTGGTATCTCATACGCGATCAACAGCGGCTACCATTCATGGGGACCGCTCTTTGGC 3060
Qy       1014 LysLeuPhePheAlaPheTrpValIleValHisLeuTyrProPheLeuLysGlyLeuMet 1033
Db       3061 AAGCTCTTCTTTGCCTTCTGGGTGATTGTCCACTTGTACCCCTTCCTCAAGGGTCTTATG 3120
Qy       1034 GlyArgGlnAsnArgThrProThrIleValIleValTrpAlaValLeuLeuAlaSerIle 1053
Db       3121 GGTCGGCAAAACCGCACTCCGACCATCGTTGTTGTTTGGGCAATCCTTCTGGCTTCGATC 3180
Qy       1054 PheSerLeuLeuTrpValArgValAspProPheThrThrArgLeuAlaGlyProAsnIle 1073
Db       3181 TTCTCATTGCTGTGGGTTCGCATCGATCCATTCACCACCCGTGTCACCGGCCCAGATACC 3240
Qy       1074 GlnThrCysGlyIleAsnCys 1080
Db       3241 CAAACATGTGGCATCAACTGC 3261
```

RESULT 2
AAS16458
ID AAS16458 standard; cDNA; 3799 BP.
XX
AC AAS16458;
XX
DT 14-FEB-2002 (first entry)
XX
DE Corn cDNA encoding cellulose synthase Cqrae19/cesA-19.
XX
KW Corn; ss; cellulose synthase; Cdpgs45; cesA-3; Cqrae19; cesA-9;
KW stalk quality; improved stand; silage; pericarp; kernel hardening;
KW handling ability; transgenic plant.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
FT CDS 238. .3799
FT /*tag= a
FT /product= "Cellulose synthase"
XX
PN WO200179516-A2.
XX
PD 25-OCT-2001.
XX
PF 12-APR-2001; 2001WO-US011951.
XX
PR 14-APR-2000; 2000US-00550483.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Dhugga KS, Helentjaris TG;
XX
DR WPI; 2002-041338/05.
DR P-PSDB; AAU10496.
XX
PT New cellulose synthase polypeptides and polynucleotides, useful in
PT improving stalk quality or silage, and in increasing concentration of
PT cellulose in the pericarp, hardening the kernel for improved handling
PT ability.
XX
PS Claim 4; Page 80-85; 88pp; English.
XX
CC The invention relates to isolated nucleic acids encoding two cellulose

CC synthase proteins from corn, Cdpgs45 (cesA-3) and Cqrael9 (cesA-9). Also
CC disclosed are a recombinant expression cassette comprising the
CC polynucleotide (operably linked to a promoter) a host cell comprising the
CC recombinant expression cassette and a transgenic plant comprising the
CC recombinant expression cassette. The nucleic acid is useful in the
CC improvement of stalk quality for improved stand or silage, and in the
CC increased concentration of cellulose in the pericarp, hardening the
CC kernel, and thus improving its handling ability. The nucleic acids may
CC also be used as probes or amplification primers in the detection,
CC quantification or isolation of gene transcripts, as probes in detecting
CC deficiencies in the level of mRNA, for detecting gene mutations or
CC allelic variants, for monitoring up regulation of expression or changes
CC in enzyme activity in screening assays, for site directed mutagenesis,
CC and in sense or antisense suppression of one or more genes in a host
CC cell, tissue or plant. The polypeptides may be used in assays for enzyme
CC agonists or antagonists, and as immunogen or antigen to obtain antibodies
CC specifically immunoreactive with the protein. The present sequence
CC encodes a corn cellulose synthase of the invention
XX
SQ Sequence 3799 BP; 925 A; 931 C; 995 G; 944 T; 0 U; 4 Other;

Alignment Scores:

Pred. No.:	0	Length:	3799
Score:	5423.50	Matches:	996
Percent Similarity:	96.48%	Conservative:	46
Best Local Similarity:	92.22%	Mismatches:	37
Query Match:	93.86%	Indels:	1
DB:	6	Gaps:	1

US-09-900-237A-30 (1-1080) x AAS16458 (1-3799)

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Qy          1 MetAspGlyAspAlaAspAlaLeuLysSerGlyArgHisGlyAlaGlyAspValCysGln 20
              |||:::|||||||||||||   :::|||||||||||   |||   |||   |||||||||
Db        238 ATGGAGGGCGACGCGGACGGCGTGAAGTCGGGGAGGCGCGGGGGAGGGCAGGTGTGCCAG 297

Qy         21 IleCysAlaAspGlyLeuGlyThrThrLeuAspGlyAspValPheThrAlaCysAspVal 40
              ||||||   ||||||:::|||||||||   :::|||||||||||||||||||||||||||
Db        298 ATCTGCGGCGATGGCGTGGGCACTACGGCGGAGGGAGACGTCTTCACCGCCTGCGACGTC 357

Qy         41 CysArgProProValCysArgProCysTyrGluHisGluArgLysGluGlyThrGlnAla 60
              |||  ||||||||||||||||||||||||||:::|||||||:::|||||||||||||||
Db        358 TGCGGGTTCCCGGTGTGCCGCCCCTGCTACGAGTACGAGCGCAAGGACGGCACACAAGCG 417

Qy         61 CysLeuGlnCysLysThrLysTyrLysArgHisArgGlySerProAlaIleArgGlyGlu 80
              |||   |||||||||   |||||||||||||:::|||||||||||||||||||||||||
Db        418 TGCCCCCAGTGCAAAAACAAGTACAAGCGCCACAAGGGGAGTCCAGCGATCCGAGGGGAG 477

Qy         81 GluGlyAspAspThrAspAlaAspAspGlySerAspPheAsnTyrProAlaSerGlyThr 100
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        478 GAAGGAGACGATACTGATGCCGATGATGCTAGCGACTTCAACTACCCTGCATCTGGCAAT 537

Qy        101 GluAspGlnLysGlnLysIleAlaAspArgMetArgSerTrpArgMetAsnThrGlyGly 120
              :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 GACGACCAGAAGCAGAAGATTGCTGACAGGATGCGCAGCTGGCGCATGAATGCTGGGGGC 597

Qy        121 SerGlyAsnValGlyHisProLysTyrAspSerGlyGluIleGlyLeuSerLysTyrAsp 140
              ||||||:::||||||   ||||||||||||||||||||||||||:::|||||||||||||
Db        598 AGCGGGGATGTTGGCCGCCCCAAGTATGACAGTGGTGAGATCGGGCTTACCAAGTACGAC 657

Qy        141 SerGlyGluIleProArgGlyTyrValProSerValThrAsnSerGlnMetSerGlyGlu 160
              |||||||||||||||||||||:::|||||||||||||||||||||||:::||||||||||
Db        658 AGTGGTGAGATCCCTCGGGGATACATCCCGTCAGTCACTAACAGCCAGATTTCGGGAGAA 717

Qy        161 IleProGlyAlaSerProAspHisHisMetMetSerProThrGlyAsnIleSerArgArg 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        718 ATCCCTGGTGCTTCCCCTGACCATCATATGATGTCTCCTACTGGGAACATTGGCAGGCGC 777

Qy        181 AlaProPheProTyrValAsnHisSerProAsnProSerArgGluPheSerGlySerIle 200
              ||||||||||||||:::|||||||||   ||||||||||||||||||||||||||||:::
Db        778 GCCCCATTTCCCTATATGAATCATTCATCAAATCCGTCGAGGGAATTCTCTGGTAGCGTT 837

Qy        201 GlyAsnValAlaTrpLysGluArgValAspGlyTrpLysMetLysGlnAspLysGlyAla 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        838 GGGAATGTTGCCTGGAAAGAGAGGGTTGATGGCTGGAAAATGAAGCAGGACAAGGGAACA 897

Qy        221 IleProMetThrAsnGlyThrSerIleAlaProSerGluGlyArgAlaAlaThrAspIle 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 ATTCCCATGACGAATGGCACAAGCATTGCTCCCTCTGAGGGCCGGGGTGTTGGTGATATT 957

Qy        241 AspAlaSerThrGluTyrAsnMetGluAspAlaLeuLeuAsnAspGluThrArgGlnPro 260
              ||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||||
Db        958 GATGCATCAACTGATTACAACATGGAAGATGCCTTATTAAACGATGAAACTCGCCAGCCT 1017

Qy        261 LeuSerArgLysValProIleAlaSerSerLysIleAsnProTyrArgMetValIleVal 280
              ||||||||||||||||||:::   ||||||:::|||||||||||||||||||||||||||
Db       1018 CTATCTAGGAAAGTTCCACTTCCTTCCTCCAGGATAAATCCATACAGGATGGTCATTGTG 1077

Qy        281 LeuArgLeuValValLeuSerIlePheLeuHisTyrArgLeuThrAsnProValArgAsn 300
              |||||||||:::|||||||||||||||||||||||||||||:::|||||||||||||||
Db       1078 CTACGATTGATTGTTCTAAGCATCTTCTTGCACTACCGGATCACAAATCCTGTGCGTAAT 1137

Qy        301 AlaTyrProLeuTrpLeuLeuSerValIleCysGluIleTrpPheAlaLeuSerTrpIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1138 GCATACCCACTGTGGCTTCTATCTGTTATATGTGAGATCTGGTTTGCTCTTTCCTGGATA 1197

Qy        321 LeuAspGlnPheProLysTrpPheProIleAsnArgGluThrTyrLeuAspArgLeuAla 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1198 TTGGATCAGTTTCCAAAGTGGTTTCCAATCAACCGCGAGACTTACCTTGATAGACTCGCA 1257

Qy        341 LeuArgTyrAspArgGluGlyGluProSerGlnLeuAlaAlaValAspIlePheValSer 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1258 TTAAGGTATGACCGGGAAGGTGAGCCATCTCAGTTGGCTGCTGTTGACATTTTTGTCAGT 1317

Qy        361 ThrValAspProLeuLysGluProProIleValThrAlaAsnThrValLeuSerIleLeu 380
              ||||||||||||:::|||||||||||||:::|||||||||||||||||||||||||||||
Db       1318 ACTGTCGACCCAATGAAGGAGCCTCCTCTTGTCACTGCCAATACCGTGCTATCCATTCTC 1377

Qy        381 AlaValAspTyrProValAspLysValSerCysTyrValSerAspAspGlyAlaSerMet 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db       1378 GCTGTGGACTATCCTGTGGATAAGGTCTCTTGCTATGTATCTGATGATGGAGCTGCTATG 1437

Qy        401 LeuThrPheAspAlaLeuAlaGluThrSerGluPheAlaArgLysTrpValProPheVal 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1438 CTGACATTTGATGCACTAGCTGAGACTTCAGAGTTTGCTAGAAAATGGGTGCCATTTGTT 1497

Qy        421 LysLysTyrAspIleGluProArgAlaProGluPheTyrPheCysGlnLysIleAspTyr 440
              |||||||:::|||||||||||||||||||:::|||||   ||||||||||||||||||||
Db       1498 AAGAAGTACAACATTGAACCTAGAGCTCCTGAATGGTACTTCTCCCAGAAAATTGATTAC 1557

Qy        441 LeuLysAspLysValGlnProSerPheValLysAspArgArgAlaMetLysArgGluTyr 460
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db       1558 TTGAAGGACAAAGTGCACCCTTCATTTGTTAAAGACCGCCGGGCCATGAAGAGAGAATAT 1617

Qy        461 GluGluPheLysIleArgIleAsnAlaLeuValSerLysAlaLeuLysValProGluGlu 480
              ||||||||||||||||||:::|||   ||||||:::|||||   ||||||||||||||||
Db       1618 GAAGAATTCAAAATTAGGGTAAATGGCCTTGTTGCTAAGGCACAAAAAGTCCCTGAGGAA 1677

Qy        481 GlyTrpIleMetGlnAspGlyThrProTrpProGlyAsnAsnThrArgAspHisProGly 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1678 GGATGGATCATGCAAGATGGCACACCATGGCCAGGAAACAATACCAGGGACCATCCTGGA 1737

Qy        501 MetIleGlnValPheLeuGlyHisSerGlyGlyLeuAspThrGluGlyAsnGluLeuPro 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1738 ATGATTCAGGTTTTCCTTGGTCACAGTGGTGGTCTTGATACTGAGGGTAATGAGCTACCC 1797

Qy        521 ArgLeuValTyrValSerArgGluLysArgProGlyPheGlnHisHisLysLysAlaGly 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1798 CGTTTGGTCTATGTTTCTCGTGAAAAACGTCCTGGATTCCAGCATCACAAGAAAGCTGGT 1857

Qy        541 AlaMetAsnAlaLeuValArgValSerAlaValLeuThrAsnGlyGlnTyrMetLeuAsn 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1858 GCCATGAATGCTCTTGTCCGCGTCTCAGCTGTGCTTACCAATGGACAATACATGTTGAAT 1917

Qy        561 LeuAspCysAspHisTyrIleAsnAsnSerLysAlaValArgGluAlaMetCysPheLeu 580
              ||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||||
Db       1918 CTTGATTGTGATCACTACATCAACAACAGTAAGGCTCTCAGGGAAGCTATGTGCTTCCTT 1977
```

```
Qy       581 MetAspProAsnLeuGlyProGlnValCysTyrValGlnPheProGlnArgPheAspGly 600
Db      1978 ATGGATCCTAACCTAGGAAGGAGTGTCTGCTATGTTCAGTTTCCCCAGAGGTTCGATGGT 2037

Qy       601 IleAspArgAsnAspArgTyrAlaAsnArgAsnThrValPhePheAspIleAsnLeuArg 620
Db      2038 ATTGATAGGAATGATCGATATGCCAACAGGAACACCGTGTTTTTCGATATTAACTTGAGA 2097

Qy       621 GlyLeuAspGlyIleGlnGlyProValTyrValGlyThrGlyCysValPheAsnArgThr 640
Db      2098 GGTCTTGATGGCATCCAAGGACCAGTTTATGTGGGCACTGGCTGTGTTTTCAACAGAACA 2157

Qy       641 AlaIleTyrGlyTyrGluProProIleLysAlaLysLysProGlyPheLeuAlaSerLeu 660
Db      2158 GCTCTATATGGTTATGAGCCCCCAATTAAGCAAAAGAAGGGTGGTTTCTTGTCATCACTA 2217

Qy       661 CysGlyGlyLysLysLysAlaSerLysSerLysLysArgSerSerAspLysLysLysSer 680
Db      2218 TGTGGTGGCAGGAAGAAGGGAAGCAAATCAAAGAAG---GGCTCAGACAAGAAAAAGTCA 2274

Qy       681 AsnLysHisValAspSerSerValProValPheAsnLeuGluAspIleGluGluGlyVal 700
Db      2275 CAGAAGCATGTGGACAGTTCTGTGCCAGTATTCAATCTTGAAGATATAGAGGAGGGAGTT 2334

Qy       701 GluGlyAlaGlyPheAspAspGluLysSerValLeuMetSerGlnMetSerLeuGluLys 720
Db      2335 GAAGGCGCTGGATTTGATGATGAGAAATCACTTCTTATGTCTCAAATGAGCTTGGAGAAG 2394

Qy       721 ArgPheGlyGlnSerAlaAlaPheValAlaSerThrLeuMetGluTyrGlyGlyValPro 740
Db      2395 AGATTTGGCCAATCTGCAGCTTTTGTTGCGTCCACTCTGATGGAATATGGTGGTGTTCCT 2454

Qy       741 GlnSerSerThrProGluSerLeuLeuLysGluAlaIleHisValIleSerCysGlyTyr 760
Db      2455 CAGTCTGCGACTCCAGAATCTCTTCTGAAAGAAGCTATCCATGTCATAAGTTGTGGCTAC 2514

Qy       761 GluAspLysSerGluTrpGlyThrGluIleGlyTrpIleTyrGlySerValThrGluAsp 780
Db      2515 GAGGACAAGATTGAATGGGGAACTGAGATTGGGTGGATCTATGGTTCTGTGACGGAAGAT 2574

Qy       781 IleLeuThrGlyPheLysMetHisAlaArgGlyTrpArgSerValTyrCysMetProLys 800
Db      2575 ATTCTCACTGGGTTCAAGATGCACGCACGAGGCTGGCGGTCGATCTACTGCATGCCTAAG 2634

Qy       801 ArgProAlaPheLysGlySerAlaProIleAsnLeuSerAspArgLeuAsnGlnValLeu 820
Db      2635 CGGCCGGCCTTCAAGGGATCGGCTCCCATCAATCTCTCAGACCGTCTGAACCAGGTGCTC 2694

Qy       821 ArgTrpAlaLeuGlySerValGluIleLeuPheSerArgHisCysProLeuTrpTyrGly 840
Db      2695 CGGTGGGCTCTCGGTTCAGTGGAAATCCTTTTCAGCCGGCATTGCCCCCTATGGTACGGG 2754

Qy       841 TyrGlyGlyArgLeuLysPheLeuGluArgPheAlaTyrIleAsnThrThrIleTyrPro 860
Db      2755 TACGGAGGACGCCTGAAGTTCTTGGAGAGATTCGCCTACATCAACACCACCATCTACCCG 2814

Qy       861 LeuThrSerLeuProLeuLeuValTyrCysIleLeuProAlaIleCysLeuLeuThrGly 880
Db      2815 CTCACGTCCCTCCCGCTCCTCATTTACTGTATCCTGCCTGCCATCTGCCTGCTCACGGGG 2874

Qy       881 LysPheIleMetProGluIleSerAsnLeuAlaSerIleTrpPheIleAlaLeuPheLeu 900
Db      2875 AAGTTCATCATCCCAGAGATCAGCAACTTCGCTAGTATCTGGTTCATCTCTCTCTTCATC 2934

Qy       901 SerIlePheAlaThrGlyIleLeuGluMetArgTrpSerGlyValGlyIleAspGluTrp 920
Db      2935 TCGATCTTCGCCACGGGTATCCTGGAGATGAGGTGGAGCGGCGTGGGCATCGACGAGTGG 2994

Qy       921 TrpArgAsnGluGlnPheTrpValIleGlyGlyIleSerAlaHisLeuPheAlaValPhe 940
Db      2995 TGGAGGAACGAGCAGTTCTGGGTCATCGGAGGCATCTCCGCCCACCTCTTCGCCGTCTTC 3054

Qy       941 GlnGlyLeuLeuLysValLeuAlaGlyIleAspThrAsnPheThrValThrSerLysAla 960
Db      3055 CAGGGCCTCCTCAAGGTGCTTGCCGGCATCGACACCAACTTCACCGTCACCTCCAAGGCC 3114

Qy       961 AsnAspGluGluGlyAspPheAlaGluLeuTyrMetPheLysTrpThrThrLeuLeuIle 980
Db      3115 TCGGATGAAGACGGCGACTTCGCGGAGCTGTACATGTTCAAGTGGACGACACTTCTGATC 3174

Qy       981 ProProThrThrIleLeuIleIleAsnMetValGlyValValAlaGlyThrSerTyrAla 1000
Db      3175 CCGCCCACCACCATCCTGATCATCAACCTGGTCGGCGTTGTTGCCGGCATCTCCTACGCC 3234

Qy      1001 IleAsnSerGlyTyrGlnSerTrpGlyProLeuPheGlyLysLeuPhePheAlaPheTrp 1020
Db      3235 ATCAACAGCGGGTACCAGTCGTGGGGTCCGCTCTTCGGCAAGCTCTTCTTCGCCTTCTGG 3294

Qy      1021 ValIleValHisLeuTyrProPheLeuLysGlyLeuMetGlyArgGlnAsnArgThrPro 1040
Db      3295 GTGATCGTTCACCTGTACCCGTTCCTCAAGGGTCTCATGGGTCGGCAGAACCGCACCCCG 3354

Qy      1041 ThrIleValIleValTrpAlaValLeuLeuAlaSerIlePheSerLeuLeuTrpValArg 1060
Db      3355 ACCATCGTGGTTGTCTGGGCGATCCTGCTGGCGTCGATCTTCTCCTTGCTGTGGGTTCGC 3414

Qy      1061 ValAspProPheThrThrArgLeuAlaGlyProAsnIleGlnThrCysGlyIleAsnCys 1080
Db      3415 ATCGATCCGTTCACCAACCGCGTCACTGGCCCGGATACTCGAACGTGTGGCATCAACTGC 3474
```

RESULT 3
AAZ99512
ID AAZ99512 standard; DNA; 3746 BP.
XX
AC AAZ99512;
XX
DT 03-JUL-2000 (first entry)
XX
DE DNA encoding a maize cellulose synthase.
XX
KW Maize; cellulose synthase; stalk quality; stand; silage; cellulose;
KW transgenic plant; plant breeding marker; ss.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
FT CDS 321. .3548
FT /*tag= a
FT /product= "cellulose synthase"
FT /transl_except= (pos: 1800. .1802, aa: Xaa)
FT /note= "no termination codon given; Xaa is an unspecified
FT amino acid"
XX
PN WO200009706-A2.
XX
PD 24-FEB-2000.
XX
PF 16-AUG-1999; 99WO-US018760.
XX
PR 17-AUG-1998; 98US-0096822P.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Dhugga KS, Helentjaris TG, Bowen BA, Wang X;
XX
DR WPI; 2000-224343/19.
DR P-PSDB; AAY84114.
XX
PT New genes which encode maize cellulose synthase polypeptides in plants
PT useful for modulating the expression of cellulose synthase in plants and
PT to produce transgenic plants expressing the novel protein.
XX
PS Claim 1; Page 137-141; 119pp; English.
XX
CC The present sequence encodes a maize cellulose synthase polypeptide. The

CC cellulose synthase can be used for the improvement of stalk quality for
CC improved stand or silage. It also provides an increased concentration of
CC cellulose in the pericarp, hardening the kernel and improving its
CC handling ability. The sequences are used to produce transgenic plants and
CC seeds expressing the cellulose synthase. The polynucleotide is used for
CC modulating, preferably increasing, the level of the synthase in a plant
CC cell. The plants are preferably monocots. The polynucleotide is also used
CC as a probe or primer in the detection quantitation or isolation of gene
CC transcripts. The probes are useful in detecting deficiencies in the level
CC of mRNA in screenings for desired transgenic plant, for detecting
CC mutations in the gene, for monitoring upregulation of expression or
CC changes in enzyme activity in screening assays of compounds, for
CC detection of any number of allelic variants of the gene, or for use as
CC molecular markers in plant breeding programs. The isolated nucleic acids
CC of the present invention can also be used for recombinant expression of
CC their encoded polypeptides or for use as immunogens in the preparation
CC and/or screening of antibodies. The proteins can be employed in assays
CC for enzyme agonists or antagonists of enzyme function or for use of
CC immunogens or antigens to obtain antibodies specifically immunoreactive
CC with a protein
XX
SQ Sequence 3746 BP; 861 A; 976 C; 1006 G; 902 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.:	0	Length:	3746
Score:	5421.50	Matches:	998
Percent Similarity:	96.67%	Conservative:	46
Best Local Similarity:	92.41%	Mismatches:	33
Query Match:	93.83%	Indels:	3
DB:	3	Gaps:	2

US-09-900-237A-30 (1-1080) x AAZ99512 (1-3746)

```
Qy          1 MetAspGlyAspAlaAspAlaLeuLysSerGlyArgHisGlyAlaGlyAspValCysGln 20
              |||:::|||||||||||||   :::|||||||||||   |||   |||   |||||||||
Db        321 ATGGAGGGCGACGCGGACGGCGTGAAGTCGGGGAGGCGCGGTGGCGGACAGGTGTGCCAG 380

Qy         21 IleCysAlaAspGlyLeuGlyThrThrLeuAspGlyAspValPheThrAlaCysAspVal 40
              ||||||   ||||||:::|||||||||   :::|||||||||||   ||||||||||||
Db        381 ATCTGCGGCGACGGCGTGGGCACCACGGCGGAGGGGGACGTCTTCGCCGCCTGCGACGTC 440

Qy         41 CysArgPheProValCysArgProCysTyrGluHisGluArgLysGluGlyThrGlnAla 60
              |||   |||||||||||||||||||||||||:::|||||||||:::|||||||||||||
Db        441 TGCGGGTTTCCGGTGTGCCGCCCCTGCTACGAGTACGAGCGCAAGGACGGCACGCAGGCG 500

Qy         61 CysLeuGlnCysLysThrLysTyrLysArgHisArgGlySerProAlaIleArgGlyGlu 80
              |||   |||||||||||||||||||||||||:::|||||||||||||||||||||||||
Db        501 TGCCCCCAGTGCAAGACCAAGTACAAGCGCCACAAGGGGAGCCCGGCGATCCGTGGGGAG 560

Qy         81 GluGlyAspAspThrAspAlaAspAspGlySerAspPheAsnTyrProAlaSerGlyThr 100
              ||||||||||||||||||||||      ||||||||||||||   |||||||||
Db        561 GAAGGAGACGACACTGATGCCGAT------AGCGACTTCAATTACCTTGCATCTGGCAAT 614

Qy        101 GluAspGlnLysGlnLysIleAlaAspArgMetArgSerTrpArgMetAsnThrGlyGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        615 GAGGACCAGAAGCAGAAGATTGCCGACAGAATGCGCAGCTGGCGCATGAACGTTGGGGGC 674

Qy        121 SerGlyAsnValGlyHisProLysTyrAspSerGlyGluIleGlyLeuSerLysTyrAsp 140
              ||||||:::|||||||   |||||||||||||||||||||||||||:::|||||||||
Db        675 AGCGGGGATGTTGGTCGCCCCAAGTATGACAGTGGCGAGATCGGGCTTACCAAGTATGAC 734

Qy        141 SerGlyGluIleProArgGlyTyrValProSerValThrAsnSerGlnMetSerGlyGlu 160
              |||||||||||||||||||:::|||||||||||||||||||||:::|||||||||||||
Db        735 AGTGGCGAGATTCCTCGGGGATACATCCCATCAGTCACTAACAGCCAGATCTCAGGAGAA 794

Qy        161 IleProGlyAlaSerProAspHisHisMetMetSerProThrGlyAsnIleSerArgArg 180
              |||||||||||||||||||||||||||||||||||||||||||||||||   :::|||
Db        795 ATCCCTGGTGCTTCCCCTGACCATCATATGATGTCCCCAACTGGGAACATTGGCAAGCGT 854

Qy        181 AlaProPheProTyrValAsnHisSerProAsnProSerArgGluPheSerGlySerIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        855 GCTCCATTTCCCTATGTGAACCATTCGCCAAATCCGTCAAGGGAGTTCTCTGGTAGCATT 914

Qy        201 GlyAsnValAlaTrpLysGluArgValAspGlyTrpLysMetLysGlnAspLysGlyAla 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        915 GGGAATGTTGCCTGGAAAGAGAGGGTTGATGGCTGGAAAATGAAGCAGGACAAGGGGACG 974

Qy        221 IleProMetThrAsnGlyThrSerIleAlaProSerGluGlyArgAlaAlaThrAspIle 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        975 ATTCCCATGACGAATGGCACAAGCATTGCTCCCTCTGAGGGTCGGGGTGTTGGTGATATT 1034

Qy        241 AspAlaSerThrGluTyrAsnMetGluAspAlaLeuLeuAsnAspGluThrArgGlnPro 260
              ||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||||
Db       1035 GATGCATCAACTGATTACAACATGGAAGATGCCTTATTGAACGACGAAACTCGACAGCCT 1094

Qy        261 LeuSerArgLysValProIleAlaSerSerLysIleAsnProTyrArgMetValIleVal 280
              ||||||||||||||||||:::   ||||||:::|||||||||||||||||||||||||||
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Qy        281 LeuArgLeuValValLeuSerIlePheLeuHisTyrArgLeuThrAsnProValArgAsn 300
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Qy        301 AlaTyrProLeuTrpLeuLeuSerValIleCysGluIleTrpPheAlaLeuSerTrpIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1215 GCATACCCATTATGGCTTCTATCTGTTATATGTGAGATCTGGTTTGCTCTTTCGTGGATA 1274

Qy        321 LeuAspGlnPheProLysTrpPheProIleAsnArgGluThrTyrLeuAspArgLeuAla 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1275 TTGGATCAGTTCCCTAAGTGGTTTCCAATCAACCGGGAGACGTACCTTGATAGGCTGGCA 1334

Qy        341 LeuArgTyrAspArgGluGlyGluProSerGlnLeuAlaAlaValAspIlePheValSer 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1335 TTAAGGTATGACCGGGAAGGTGAGCCATCTCAGTTGGCTGCTGTTGACATTTTCGTCAGT 1394

Qy        361 ThrValAspProLeuLysGluProProIleValThrAlaAsnThrValLeuSerIleLeu 380
              ||||||||||||:::|||||||||||:::|||||||||||||||||||||||||||||||
Db       1395 ACAGTCGACCCAATGAAGGAGCCTCCTCTTGTCACTGCCAATACCGTGCTATCCATTCTT 1454

Qy        381 AlaValAspTyrProValAspLysValSerCysTyrValSerAspAspGlyAlaSerMet 400
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Qy        401 LeuThrPheAspAlaLeuAlaGluThrSerGluPheAlaArgLysTrpValProPheVal 420
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Db       1515 CTGACATTTGATGCACTAGCTGAGACTTCAGAGTTTGCTAGAAAATGGGTACCATTTGTT 1574

Qy        421 LysLysTyrAspIleGluProArgAlaProGluPheTyrPheCysGlnLysIleAspTyr 440
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Qy        441 LeuLysAspLysValGlnProSerPheValLysAspArgArgAlaMetLysArgGluTyr 460
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Qy        461 GluGluPheLysIleArgIleAsnAlaLeuValSerLysAlaLeuLysValProGluGlu 480
              ||||||||||||:::|||:::|||   ||||||:::||||||   ||||||||||||||||
Db       1695 GAAGAATTCAAAGTTAGGGTAAATGGCCTTGTTGCTAAGGCACAGAAAGTTCCTGAGGAA 1754

Qy        481 GlyTrpIleMetGlnAspGlyThrProTrpProGlyAsnAsnThrArgAspHisProGly 500
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Db       1755 GGATGGATCATGCAAGATGGCACACCATGGCCAGGAAACAATACCMGGGACCATCCTGGA 1814

Qy        501 MetIleGlnValPheLeuGlyHisSerGlyGlyLeuAspThrGluGlyAsnGluLeuPro 520
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Qy        521 ArgLeuValTyrValSerArgGluLysArgProGlyPheGlnHisHisLysLysAlaGly 540
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Qy        541 AlaMetAsnAlaLeuValArgValSerAlaValLeuThrAsnGlyGlnTyrMetLeuAsn 560
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Db       1935 GCCATGAATGCTCTTGTTCGTGTCTCAGCTGTGCTTACCAATGGACAATACATGTTGAAT 1994

Qy        561 LeuAspCysAspHisTyrIleAsnAsnSerLysAlaValArgGluAlaMetCysPheLeu 580
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Db       1995 CTTGATTGTGATCACTACATTAACAACAGTAAGGCTCTCAGGGAAGCTATGTGCTTCCTT 2054
Qy        581 MetAspProAsnLeuGlyProGlnValCysTyrValGlnPheProGlnArgPheAspGly 600
Db       2055 ATGGACCCTAACCTAGGAAGGAGTGTCTGCTACGTCCAGTTTCCCCAGAGATTCGATGGC 2114
Qy        601 IleAspArgAsnAspArgTyrAlaAsnArgAsnThrValPhePheAspIleAsnLeuArg 620
Db       2115 ATTGACAGGAATGATCGATATGCCAACAGGAACACCGTGTTTTTCGATATTAACTTGAGA 2174
Qy        621 GlyLeuAspGlyIleGlnGlyProValTyrValGlyThrGlyCysValPheAsnArgThr 640
Db       2175 GGTCTTGATGGCATCCAAGGACCAGTTTATGTCGGAACTGGCTGTGTTTTCAACCGAACA 2234
Qy        641 AlaIleTyrGlyTyrGluProProIleLysAlaLysLysProGlyPheLeuAlaSerLeu 660
Db       2235 GCTCTATATGGTTATGAGCCCCCAATTAAGCAGAAGAAGGGTGGTTTCTTGTCATCACTA 2294
Qy        661 CysGlyGlyLysLysLysAlaSerLysSerLysLysArgSerSerAspLysLysLysSer 680
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Qy        681 AsnLysHisValAspSerSerValProValPheAsnLeuGluAspIleGluGluGlyVal 700
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Qy        701 GluGlyAlaGlyPheAspAspGluLysSerValLeuMetSerGlnMetSerLeuGluLys 720
Db       2412 GAAGGCGCTGGATTTGACGACGAGAAATCACTTCTTATGTCTCAAATGAGCCTGGAGAAG 2471
Qy        721 ArgPheGlyGlnSerAlaAlaPheValAlaSerThrLeuMetGluTyrGlyGlyValPro 740
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Qy        741 GlnSerSerThrProGluSerLeuLysGluAlaIleHisValIleSerCysGlyTyr 760
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Qy        761 GluAspLysSerGluTrpGlyThrGluIleGlyTrpIleTyrGlySerValThrGluAsp 780
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Qy        801 ArgProAlaPheLysGlySerAlaProIleAsnLeuSerAspArgLeuAsnGlnValLeu 820
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Qy        841 TyrGlyGlyArgLeuLysPheLeuGluArgPheAlaTyrIleAsnThrThrIleTyrPro 860
Db       2832 TACGGAGGGCGGCTCAAGTTCCTGGAGAGATTCGCGTACATCAACACCACCATCTACCCG 2891
Qy        861 LeuThrSerLeuProLeuLeuValTyrCysIleLeuProAlaIleCysLeuLeuThrGly 880
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Qy        901 SerIlePheAlaThrGlyIleLeuGluMetArgTrpSerGlyValGlyIleAspGluTrp 920
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Qy        921 TrpArgAsnGluGlnPheTrpValIleGlyGlyIleSerAlaHisLeuPheAlaValPhe 940
Db       3072 TGGAGGAACGAGCAGTTCTGGGTGATCGGGGGCATCTCCGCGCACCTCTTCGCCGTGTTC 3131
Qy        941 GlnGlyLeuLeuLysValLeuAlaGlyIleAspThrAsnPheThrValThrSerLysAla 960
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Qy        961 AsnAspGluGluGlyAspPheAlaGluLeuTyrMetPheLysTrpThrThrLeuLeuIle 980
Db       3192 TCGGACGAGGACGGCGACTTCGCGGAGCTGTACATGTTCAAGTGGACGACGCTCCTGATC 3251
Qy        981 ProProThrThrIleLeuIleIleAsnMetValGlyValValAlaGlyThrSerTyrAla 1000
Db       3252 CCGCCCACCACCATCCTGATCATCAACCTGGTCGGCGTCGTCGCCGGCATCTCCTACGCC 3311
Qy       1001 IleAsnSerGlyTyrGlnSerTrpGlyProLeuPheGlyLysLeuPhePheAlaPheTrp 1020
Db       3312 ATCAACAGCGGATACCAGTCGTGGGGCCCGCTCTTCGGCAAGCTCTTCTTCGCCTTCTGG 3371
Qy       1021 ValIleValHisLeuTyrProPheLeuLysGlyLeuMetGlyArgGlnAsnArgThrPro 1040
Db       3372 GTCATCGTCCACCTGTACCCGTTCCTCAAGGGCCTCATGGGCAGGCAGAACCGCACCCCG 3431
Qy       1041 ThrIleValIleValTrpAlaValLeuLeuAlaSerIlePheSerLeuLeuTrpValArg 1060
Db       3432 ACCATCGTCGTCGTCTGGGCCATCCTGCTGGCGTCCATCTTCTCCTTGCTGTGGGTTCGC 3491
Qy       1061 ValAspProPheThrThrArgLeuAlaGlyProAsnIleGlnThrCysGlyIleAsnCys 1080
Db       3492 ATCGACCCCTTCACCACCCGCGTCACTGGCCCGGATACCCAGACGTGTGGCATCAACTGC 3551
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RESULT 4
AAZ99527
ID AAZ99527 standard; DNA; 3746 BP.
XX
AC AAZ99527;
XX
DT 03-JUL-2000 (first entry)
XX
DE DNA encoding a maize cellulose synthase.
XX
KW Maize; cellulose synthase; stalk quality; stand; silage; cellulose;
KW transgenic plant; plant breeding marker; ss.
XX
OS Zea mays.
XX
FH Key   Location/Qualifiers
FT CDS   321. .3449
FT   /*tag= a
FT   /product= "cellulose synthase"
FT   /transl_except= (pos: 1800. .1802, aa: Xaa)
FT   /note= "no termination codon given; Xaa is an unspecified
FT   amino acid"
XX
PN WO200009706-A2.
XX
PD 24-FEB-2000.
XX
PF 16-AUG-1999; 99WO-US018760.
XX
PR 17-AUG-1998; 98US-0096822P.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Dhugga KS, Helentjaris TG, Bowen BA, Wang X;
XX
DR WPI; 2000-224343/19.
DR P-PSDB; AAY84119.
XX
PT New genes which encode maize cellulose synthase polypeptides in plants
PT useful for modulating the expression of cellulose synthase in plants and
PT to produce transgenic plants expressing the novel protein.
XX
PS Claim 1; Page 176-181; 119pp; English.